

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
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Application Serial Number: 10/523,982  
Source: PCT/  
Date Processed by STIC: 2/13/06

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 02/13/2006

PATENT APPLICATION: US/10/523,982

TIME: 13:13:02

Input Set : A:\Sequence Listing 9-9-05 2005\_0199A.txt

Output Set: N:\CRF4\02132006\J523982.raw

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3 <110> APPLICANT: KAKIZUKA, Akira
4     KAMEI, Yasutomi
5     OHIZUMI, Hiroshi
7 <120> TITLE OF INVENTION: A method of drug screening
9 <130> FILE REFERENCE: 2005-0199A/WMC/00653
11 <140> CURRENT APPLICATION NUMBER: 10/523,982
12 <141> CURRENT FILING DATE: 2005-02-08
14 <150> PRIOR APPLICATION NUMBER: PCT/JP2003/010163
15 <151> PRIOR FILING DATE: 2003-08-08
17 <150> PRIOR APPLICATION NUMBER: JP 2002-231999
18 <151> PRIOR FILING DATE: 2002-08-08
20 <160> NUMBER OF SEQ ID NOS: 2
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 3345
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (32)..(3076)
33 <400> SEQUENCE: 1
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35                               Met Ala Gly Asn Asp Cys Gly
36                               1           5
38 gcg ctg ctg gat gaa gag ctc tcg tcc ttc ttc ctc aac tat ctc tct      100
39 Ala Leu Leu Asp Glu Glu Leu Ser Ser Phe Phe Leu Asn Tyr Leu Ser
40       10           15           20
42 gac acg cag ggt ggg gac tct gga gag gaa cag ctg tgt gct gac ttg      148
43 Asp Thr Gln Gly Gly Asp Ser Gly Glu Glu Gln Leu Cys Ala Asp Leu
44       25           30           35
46 cca gag ctt gac ctc tcc cag ctg gac gcc agt gac ttt gac tca gcc      196
47 Pro Glu Leu Asp Leu Ser Gln Leu Asp Ala Ser Asp Phe Asp Ser Ala
48 40           45           50           55
50 acg tgc ttt ggg gag ctg cag tgg tgc ccg gag acc tca gag aca gag      244
51 Thr Cys Phe Gly Glu Leu Gln Trp Cys Pro Glu Thr Ser Glu Thr Glu
52       60           65           70
54 ccc agc cag tac agc ccc gat gac tcc gag ctc ttc cag att gac agt      292
55 Pro Ser Gln Tyr Ser Pro Asp Asp Ser Glu Leu Phe Gln Ile Asp Ser
56       75           80           85
58 gag aat gaa gct ctc ttg gct gcg ctt acg aag acc ctg gat gac atc      340
59 Glu Asn Glu Ala Leu Leu Ala Ala Leu Thr Lys Thr Leu Asp Asp Ile
60       90           95           100
62 ccc gaa gac gat gtg ggg ctg gct gcc ttc cca gaa ctg gat gaa ggc      388

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63 Pro Glu Asp Asp Val Gly Leu Ala Ala Phe Pro Glu Leu Asp Glu Gly
64      105                      110                      115
66 gac aca cca tcc tgc acc cca gcc tca cct gcc ccc tta tct gca ccc 436
67 Asp Thr Pro Ser Cys Thr Pro Ala Ser Pro Ala Pro Leu Ser Ala Pro
68 120                      125                      130                      135
70 ccc agc ccc acc ctg gag agg ctt ctg tcc cca gcg tct gac gtg gac 484
71 Pro Ser Pro Thr Leu Glu Arg Leu Leu Ser Pro Ala Ser Asp Val Asp
72      140                      145                      150
74 gag ctt tca ctg cta cag aag ctc ctc ctg gcc aca tcc tcc cca aca 532
75 Glu Leu Ser Leu Leu Gln Lys Leu Leu Leu Ala Thr Ser Ser Pro Thr
76      155                      160                      165
78 gca agc tct gac gct ctg aag gac ggg gcc acc tgg tcc cag acc agc 580
79 Ala Ser Ser Asp Ala Leu Lys Asp Gly Ala Thr Trp Ser Gln Thr Ser
80      170                      175                      180
82 ctc agt tcc aga agt cag cgg cct tgt gtc aag gtg gat ggc acc cag 628
83 Leu Ser Ser Arg Ser Gln Arg Pro Cys Val Lys Val Asp Gly Thr Gln
84      185                      190                      195
86 gat aag aag acc ccc aca ctg cgg gct cag agc cgg cct tgt acg gaa 676
87 Asp Lys Lys Thr Pro Thr Leu Arg Ala Gln Ser Arg Pro Cys Thr Glu
88 200                      205                      210                      215
90 ctg cat aag cac ctc act tcg gtg ctg ccc tgt ccc aga gtg aaa gcc 724
91 Leu His Lys His Leu Thr Ser Val Leu Pro Cys Pro Arg Val Lys Ala
92      220                      225                      230
94 tgc tcc cca act ccg cac ccg agc cct cgg ctc ctc tcc aaa gag gag 772
95 Cys Ser Pro Thr Pro His Pro Ser Pro Arg Leu Leu Ser Lys Glu Glu
96      235                      240                      245
98 gag gag gag gtg ggg gag gat tgc cca agc cct tgg ctg act cca gcc 820
99 Glu Glu Glu Val Gly Glu Asp Cys Pro Ser Pro Trp Leu Thr Pro Ala
100      250                      255                      260
102 tcg ccc caa gac tcc cta gca cag gac acg gcc agc ccc gac agt gcc 868
103 Ser Pro Gln Asp Ser Leu Ala Gln Asp Thr Ala Ser Pro Asp Ser Ala
104      265                      270                      275
106 cag cct ccc gag gag gat gtg agg gcc atg gta cag ctc att cgc tac 916
107 Gln Pro Pro Glu Glu Asp Val Arg Ala Met Val Gln Leu Ile Arg Tyr
108 280                      285                      290                      295
110 atg cat acc tac tgc ctg cct cag agg aag ctg ccc caa cgg gcc cca 964
111 Met His Thr Tyr Cys Leu Pro Gln Arg Lys Leu Pro Gln Arg Ala Pro
112      300                      305                      310
114 gag cca atc ccc cag gcc tgc agc agc ctc tcc agg cag gtt caa ccc 1012
115 Glu Pro Ile Pro Gln Ala Cys Ser Ser Leu Ser Arg Gln Val Gln Pro
116      315                      320                      325
118 cga tcc cgg cat ccc ccc aaa gcc ttc tgg act gag ttc tct atc cta 1060
119 Arg Ser Arg His Pro Pro Lys Ala Phe Trp Thr Glu Phe Ser Ile Leu
120      330                      335                      340
122 agg gaa ctt ctg gcc caa gat atc ctc tgt gat gtt agc aag ccc tac 1108
123 Arg Glu Leu Leu Ala Gln Asp Ile Leu Cys Asp Val Ser Lys Pro Tyr
124      345                      350                      355
126 cgc ctg gcc ata cct gtc tat gct tcc ctc aca cct cag tcc agg ccc 1156
127 Arg Leu Ala Ile Pro Val Tyr Ala Ser Leu Thr Pro Gln Ser Arg Pro

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128	360																
130	agg	ccc	ccc	aag	gac	agt	cag	gcc	tcc	cct	gcc	cac	tct	gcc	atg	gca	1204
131	Arg	Pro	Pro	Lys	Asp	Ser	Gln	Ala	Ser	Pro	Ala	His	Ser	Ala	Met	Ala	
132					380						385				390		
134	gaa	gag	gtg	aga	atc	act	gct	tcc	ccc	aag	agc	acc	ggg	cct	aga	ccc	1252
135	Glu	Glu	Val	Arg	Ile	Thr	Ala	Ser	Pro	Lys	Ser	Thr	Gly	Pro	Arg	Pro	
136					395					400				405			
138	agc	ctg	cgt	cct	ctg	agg	ctg	gag	gtg	aaa	cgg	gat	gtt	aac	aag	cct	1300
139	Ser	Leu	Arg	Pro	Leu	Arg	Leu	Glu	Val	Lys	Arg	Asp	Val	Asn	Lys	Pro	
140				410					415				420				
142	aca	agg	caa	aag	cgg	gag	gaa	gat	gag	gag	gag	gag	gag	gaa	gaa	gaa	1348
143	Thr	Arg	Gln	Lys	Arg	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	
144				425				430				435					
146	gaa	gag	gaa	gaa	gaa	aaa	gaa	gag	gaa	gaa	gag	gag	tgg	ggc	agg	aag	1396
147	Glu	Glu	Glu	Glu	Glu	Lys	Glu	Glu	Glu	Glu	Glu	Glu	Trp	Gly	Arg	Lys	
148	440					445					450					455	
150	aga	cca	ggg	cgt	ggc	ctg	cca	tgg	acc	aaa	cta	ggg	agg	aag	atg	gac	1444
151	Arg	Pro	Gly	Arg	Gly	Leu	Pro	Trp	Thr	Lys	Leu	Gly	Arg	Lys	Met	Asp	
152					460					465				470			
154	agc	ccc	gtg	tgc	ccc	gtg	cgg	cgc	tcc	agg	aga	ctg	aat	cca	gag	ctg	1492
155	Ser	Ser	Val	Cys	Pro	Val	Arg	Arg	Ser	Arg	Arg	Leu	Asn	Pro	Glu	Leu	
156					475				480					485			
158	ggg	ccc	tgg	ctg	aca	ttc	act	gat	gag	ccc	tta	ggg	gct	ctg	ccc	tcg	1540
159	Gly	Pro	Trp	Leu	Thr	Phe	Thr	Asp	Glu	Pro	Leu	Gly	Ala	Leu	Pro	Ser	
160					490				495				500				
162	atg	tgc	ctg	gat	aca	gag	acc	cac	aac	ctg	gag	gaa	gac	ctg	ggc	agc	1588
163	Met	Cys	Leu	Asp	Thr	Glu	Thr	His	Asn	Leu	Glu	Glu	Asp	Leu	Gly	Ser	
164				505				510				515					
166	ctc	aca	gac	agt	agt	caa	ggc	cgg	cag	ctc	ccc	cag	gga	tcc	cag	atc	1636
167	Leu	Thr	Asp	Ser	Ser	Gln	Gly	Arg	Gln	Leu	Pro	Gln	Gly	Ser	Gln	Ile	
168	520					525					530					535	
170	ccc	gcc	ctg	gaa	agc	ccc	tgt	gag	agt	ggg	tgc	gga	gac	aca	gat	gaa	1684
171	Pro	Ala	Leu	Glu	Ser	Pro	Cys	Glu	Ser	Gly	Cys	Gly	Asp	Thr	Asp	Glu	
172					540					545					550		
174	gat	cca	agc	tgc	cca	cag	ccc	act	tcc	aga	gac	tcc	tcc	agg	tgc	ctc	1732
175	Asp	Pro	Ser	Cys	Pro	Gln	Pro	Thr	Ser	Arg	Asp	Ser	Ser	Arg	Cys	Leu	
176					555				560								

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194	gag gct ctt ccg ctc aca gcc acc cca gga gct tcc cac aag ctg ccc	1972
195	Glu Ala Leu Pro Leu Thr Ala Thr Pro Gly Ala Ser His Lys Leu Pro	
196	635 640 645	
198	aag agg cac cca gag cga agc gag ctc ctg tcc cat ttg cag cat gcc	2020
199	Lys Arg His Pro Glu Arg Ser Glu Leu Leu Ser His Leu Gln His Ala	
200	650 655 660	
202	aca acc caa cca gtc tca cag gct ggc cag aag cgc ccc ttc tcc tgc	2068
203	Thr Thr Gln Pro Val Ser Gln Ala Gly Gln Lys Arg Pro Phe Ser Cys	
204	665 670 675	
206	tcc ttt gga gac cac gac tac tgc cag gtg ctc agg cca gag gct gcc	2116
207	Ser Phe Gly Asp His Asp Tyr Cys Gln Val Leu Arg Pro Glu Ala Ala	
208	680 685 690 695	
210	ctg cag agg aag gtg ctg cgg tcc tgg gag cca atc ggg gtc cac ctt	2164
211	Leu Gln Arg Lys Val Leu Arg Ser Trp Glu Pro Ile Gly Val His Leu	
212	700 705 710	
214	gaa gac ttg gcc cag cag ggt gcc cct ctg cca acg gaa aca aag gcc	2212
215	Glu Asp Leu Ala Gln Gln Gly Ala Pro Leu Pro Thr Glu Thr Lys Ala	
216	715 720 725	
218	cct agg agg gag gaa aac cag aac tgt gac cct acc cac aag gac agc	2260
219	Pro Arg Arg Glu Ala Asn Gln Asn Cys Asp Pro Thr His Lys Asp Ser	
220	730 735 740	
222	atg cag cta aga gac cat gag atc cgt gcc agt ctc aca aag cac ttt	2308
223	Met Gln Leu Arg Asp His Glu Ile Arg Ala Ser Leu Thr Lys His Phe	
224	745 750 755	
226	ggg ctg ctg gag act gct ctg gaa ggt gaa gac ctg gcg tcc tgt aaa	2356
227	Gly Leu Leu Glu Thr Ala Leu Glu Gly Glu Asp Leu Ala Ser Cys Lys	
228	760 765 770 775	
230	agc ccg gag tat gac acc gta ttt gag gac agc agc agc agc agt ggc	2404
231	Ser Pro Glu Tyr Asp Thr Val Phe Glu Asp Ser Ser Ser Ser Ser Gly	
232	780 785 790	
234	gag agt agc ttc ctg ctt gag gag gag gag gaa gag gag gag gga ggg	2452
235	Glu Ser Ser Phe Leu Leu Glu Glu Glu Glu Glu Glu Glu Gly Gly	
236	795 800 805	
238	gaa gag gac gat gaa gga gag gac tca ggg gtc agc cct ccc tgc tct	2500
239	Glu Glu Asp Asp Glu Gly Glu Asp Ser Gly Val Ser Pro Pro Cys Ser	
240	810 815 820	
242	gat cac tgc ccc tac cag agc cca ccc agt aag gcc agt cgg cag ctc	2548
243	Asp His Cys Pro Tyr Gln Ser Pro Pro Ser Lys Ala Ser Arg Gln Leu	
244	825 830 835	
246	tgc tcc cga agc cgc tcc agt tcc ggc tcc tcg tcc tgc agc tcc tgg	2596
247	Cys Ser Arg Ser Arg Ser Ser Ser Gly Ser Ser Ser Cys Ser Ser Trp	
248	840 845 850 855	
250	tca cca gcc acc cgg aag aac ttc aga cgt gag agc aga ggg ccc tgt	2644
251	Ser Pro Ala Thr Arg Lys Asn Phe Arg Arg Glu Ser Arg Gly Pro Cys	
252	860 865 870	
254	tca gat gga acc cca agc gtc cgg cat gcc agg aag cgg cgg gaa aag	2692
255	Ser Asp Gly Thr Pro Ser Val Arg His Ala Arg Lys Arg Arg Glu Lys	
256	875 880 885	
258	gcc atc ggt gaa ggc cgt gtg gta tac att cga aat ctc tcc agt gac	2740

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259 Ala Ile Gly Glu Gly Arg Val Val Tyr Ile Arg Asn Leu Ser Ser Asp
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263 Met Ser Ser Arg Glu Leu Lys Lys Arg Phe Glu Val Phe Gly Glu Ile
264      905      910      915
266 gta gag tgc cag gtg ctg acg aga agt aaa aga ggc cag aag cac ggt 2836
267 Val Glu Cys Gln Val Leu Thr Arg Ser Lys Arg Gly Gln Lys His Gly
268 920      925      930      935
270 ttt atc acc ttc cgg tgt tca gag cac gct gcc ctg tcc gtg agg aac 2884
271 Phe Ile Thr Phe Arg Cys Ser Glu His Ala Ala Leu Ser Val Arg Asn
272      940      945      950
274 ggc gcc acc ctg aga aag cgc aat gag ccc tcc ttc cac ctg agc tat 2932
275 Gly Ala Thr Leu Arg Lys Arg Asn Glu Pro Ser Phe His Leu Ser Tyr
276      955      960      965
278 gga ggg ctc cgg cac ttc cgt tgg ccc aga tac act gac tat gat ccc 2980
279 Gly Gly Leu Arg His Phe Arg Trp Pro Arg Tyr Thr Asp Tyr Asp Pro
280      970      975      980
282 aca tct gag gag tcc ctt ccc tca tct ggg aaa agc aag tac gaa gcc 3028
283 Thr Ser Glu Glu Ser Leu Pro Ser Ser Gly Lys Ser Lys Tyr Glu Ala
284      985      990      995
286 atg gat ttt gac agc tta ctg aaa gag gcc cag cag agc ctg cat tga 3076
287 Met Asp Phe Asp Ser Leu Leu Lys Glu Ala Gln Gln Ser Leu His
W--> 288 1000      1005      1010      1015
290 tatcagcctt aaccttcgag gaatacctca atacctcaga caaggccctt ccaatatgtt 3136
292 tacgttttca aagaaaagag tatatgagaa ggagagcgag cgagcgagcg agcgagcgag 3196
294 tgagcgtgag agatcacaca ggagagagaa agacttgaat ctgctgtcgt ttcctttaaa 3256
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298 atccccgggtg gcatccctgt gacccctcc 3345
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303 <212> TYPE: PRT
304 <213> ORGANISM: Homo sapiens
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309 Phe Phe Leu Asn Tyr Leu Ser Asp Thr Gln Gly Gly Asp Ser Gly Glu
310 20 25 30
311 Glu Gln Leu Cys Ala Asp Leu Pro Glu Leu Asp Leu Ser Gln Leu Asp
312 35 40 45
313 Ala Ser Asp Phe Asp Ser Ala Thr Cys Phe Gly Glu Leu Gln Trp Cys
314 50 55 60
315 Pro Glu Thr Ser Glu Thr Glu Pro Ser Gln Tyr Ser Pro Asp Asp Ser
316 65 70 75 80
317 Glu Leu Phe Gln Ile Asp Ser Glu Asn Glu Ala Leu Leu Ala Ala Leu
318 85 90 95
319 Thr Lys Thr Leu Asp Asp Ile Pro Glu Asp Asp Val Gly Leu Ala Ala
320 100 105 110
321 Phe Pro Glu Leu Asp Glu Gly Asp Thr Pro Ser Cys Thr Pro Ala Ser
322 115 120 125

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**VERIFICATION SUMMARY**

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Input Set : **A:\Sequence Listing 9-9-05 2005\_0199A.txt**

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L:288 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1